Blocking:
How to get a more precise estimate without increasing sample size

Fisher's 3 principles of experimental design:
Randomization
Replication
Local control of variability
= Blocking

A framework for the issues: Two sample comparison, Problem: required n too large
Error variance (among observations) = $\sigma_e^2 = \sigma_{subjects}^2 + \sigma_{measurements}^2$
How can you reduce σ_e^2?
More precise measurements, reduce $\sigma_{measurements}^2$
Often hard (slower to make a measurement or requires more expensive equipment)
Reduce variability among subjects in same treatment $\Rightarrow$ smaller $\sigma_{subjects}^2$
narrow the study population:
residents of Story Co. $\Rightarrow$ .. and Men, 30 - 35
only informs you about that narrower study population
create groups of similar individuals
Men 30-35, Men 40-45, Women 20-25
Informs you about more heterogeneous population

Blocking:
create groups of similar individuals
randomly assign treatment **within each block**
Named and popularized by RA Fisher
Examples using a field study: 3 treatments, 4 reps, eu = plot

Completely Randomized Design (CRD):
picture of the field layout

Randomized Complete Block Design (RCBD):
picture of the field layout

Vocabulary:
- Complete Blocks:
  - every treatment occurs at least one in every block
    - some treatments may occur multiple times in a block
- Incomplete blocks:
  - each block only has a subset of treatments
  - Baking cakes example
  - usually, arrangement of subsets into blocks carefully done
- Block size:
  - # experimental units (plots, subjects) within each block

Practical detail: consider complete blocks,
- Each treatment requires a plot in a field study, a person, or some other eu
- Small blocks are more homogeneous than large blocks
  - Men 30-35 more homogeneous than Men 30-49
  - $\Rightarrow$ want smallest possible block size
  - + complete $\Rightarrow$ one and only one of each trt in a block
- Plant breeding, often comparing 400+ varieties
  - Uses all sorts of incomplete block designs
    - alpha-lattice, row-column designs, spatial adjustments

Usual model, 1 of each trt in each block:

$$Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$$

- T treatments, B blocks $\Rightarrow$ $T\,B$ observations
  - τ_i: treatment effects (deviations from μ), i: treatment
  - β_j: block effects (deviations from μ), j: block
- Assumes treatment effects and block effects are additive
  - $\tau_2 - \tau_1$ same in each block

Handout on ANOVA tables:
- Two ways to compute data-dependent quantities
  - formulae: equal sample sizes, no missing data
  - model comparison: any data

Skeleton ANOVA table:
- the parts of the ANOVA table that do not depend on data
  - do depend on the design
- equivalent to the model equation, but often easier to interpret

RCBD: B blocks, T treatments
- skeleton ANOVA

Source	df
Blocks	B-1
Treatments	T-1
error	(B-1)(T-1)
c.total	BT-1

Quantities of interest:
- trt. mean: $\overline{Y}_{i.}$, obs. in trt i averaged over blocks
- pooled sd: $s = \sqrt{MSE}$, MSE = Mean Square Error from ANOVA
- se trt diff: $\text{se}(\overline{Y}_{i.} - \overline{Y}_{k.}) = s\sqrt{2/B}$
- se trt mean: depends on a detail of the model:
  - are block effects a fixed effect or a random effect?
  - more about this choice soon
- F test for no differences among trt means: MS(Treatments) / MS(Error)

Example: plant study
- Response is growth over 2 weeks
- 3 treatments (control, T1, T2) to improve growth
- block = group of 3 plants with similar size at start
  - one plant per pot,
  - pots in a block places next to each other on bench
- Results from RCBD (correct) and ignoring blocks (CRD)

	Group averages				se trt
Analysis	C	T1	T2	$s = \sqrt{MSE}$	diff
RCBD	7.2	8.9	10.4	1.91	0.86
CRD	7.2	8.9	10.4	2.28	1.02

Comparing designs by comparing sample sizes
- Various ways to quantify "how much better is design B?"
- I find comparing sample sizes to be the most interpretable
- Using 10 blocks, we get se trt diff = 0.86
- If you didn't use blocks ($s = 2.28$), with 10 replicates, get se trt diff = 1.02
  - how many replicates would need to force se trt diff down to 0.86?
    - Solve $0.86 = 2.28\sqrt{2/n}$ for n, get $n = 13.5$ (i.e., 14 per trt)
  - RCBD: total of 30 plants. CRD requires 42 plants to get same se trt diff
- get 12 plants total "for free' by blocking

Understanding what blocking is actually doing
- Numerical example: 2 blocks, 3 treatments
  - The data:

Block	Trt A	Trt B	Trt C
1	5	8	15
2	10	9	13

1) Using models: "pulling out consistent effect from the error"

$$\text{RCDB:} \quad Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$$
$$\text{CRD:} \quad Y_{ij} = \mu + \tau_i + \varepsilon^*_{ij}$$

ε^*_{ij} in CRD $= \beta_j + \varepsilon_{ij}$ in RCBD
Numerical example, fitting RCBD (one possible set of estimates):
$\hat{\mu} = 9$, $\hat{\beta} = -0.67,\ 0.67$ $\hat{\tau} = -2.5,\ -1.5,\ 4.0$
The RCBD residuals, $\hat{\varepsilon}_{ij}$:

Block	Trt A	Trt B	Trt C
1	-1.83	0.17	1.67
2	1.83	-0.17	-1.67

The CRD residuals, $\hat{\varepsilon}^*_{ij}$

Block	Trt A	Trt B	Trt C
1	-2.5 = -1.83 + -0.67	-0.5 = 0.17 + -0.67	1.0 = 1.67 + -0.67
2	2.5 = 1.85 + 0.67	0.5 = -0.17 + 0.67	-1.0 = -1.67 + 0.67

block analysis "pulls out" consistent effect (β_j) shared by all obs in a block
2) using models: consistency of trt effects across blocks
RCBD: error term quantifies consistency (or lack of) trt diff across blocks
σ^2_{error} small, all ε_{ij} close to 0:
$C - T1$ (and $C - T2$ and $T1 - T2$) similar in all blocks $\Rightarrow$ consistent
σ^2_{error} large, at least some ε_{ij} large (+ or $-$):
$C - T1$ (or $C - T2$ or $T1 - T2$) different in all blocks $\Rightarrow$ not consistent
Numerical example, all treatment differences computed within each block

Block	B- A	C -A	C - B
1	3	10	7
2	-1	3	4
ave	1	6.5	5.5

Here, not especially consistent

3) Using models: "adjusting for block effects"

$$Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$$

block average for block j: $= \hat{\mu} + \hat{\beta}_j$: 9.33, 10.67

$$Y_{ij} - (\hat{\mu} + \hat{\beta}_j) = \tau_i + \varepsilon_{ij}$$

Observations "adjusted" for block averages

Block	B- A	C -A	C - B
1	-4.33	-1.33	5.67
2	-0.67	-1.67	2.33
ave	-2.5	-1.5	4

Review of ANOVA tables:

each line corresponds to one term in the model equation

for an RCBD: $\tau \Rightarrow$ Treatment, $\beta \Rightarrow$ Block, $\varepsilon \Rightarrow$ Error

df associated with each term, in a "standard model" that include the intercept

Main effects: df = # levels - 1

Treament: 3 levels, 2 df

Block: 2 levels, 1 df

Interaction effects, e.g., A*B (SAS,JMP) or A:B (R):

df = # combinations - (df for A + df for B - 1)

Often = (df for A) * (df for B). Does not occur when some combinations of A and B are missing

no interactions in the current model, will see later

Residual Error: # observations - 1 - sum of all other df

Here, 6 observations, error df = 6 - 1 - (2 + 1) = 2

Also = 2 * 1 = 2

Corrected total: # obs - 1

Why -1? Why "corrected"?

Because we have removed the effect of the intercept (μ)

We don't care whether the overall average is 10 or 100

That overall average is accounted for by the intercept

Using an ANOVA table to understand what blocking is doing:

Plant study (3 treatments, 10 blocks)

Compare ANOVA table for RCBD to that for CRD

RCBD				CRD			
Source	df	SS	MS	Source	df	SS	MS
Trt	2	51.3	25.6	Trt	2	51.3	25.6
Blocks	9	74.8	8.3				
Error	18	66.1	3.7	Error	27	140.9	5.2
c.total	29			c.total	29		

Pooled error variance = MSE,

pooled error sd = $\sqrt{\text{MSE}}$ often called rMSE

Here, RCBD rMSE = $\sqrt{3.7} = 1.92$,

CRD rMSE = $\sqrt{5.2} = 2.28$

se trt diff = rMSE $\sqrt{2/n}$

Here $n = 10$, RCBD se = $1.92\ \sqrt{2/10} = 0.86$,

CRD se = $2.28\ \sqrt{2/10} = 1.02$